

FIGURE 1

hEGFH2 seq	1	MPTDHEEPCGPSHKSFCNLGGLCYVIPTIPSPFCRCVENYTGARCEEVFLP	51
mEGFH2 seq	1	MPTDHEQPCGPRHRSFCNLGGICYVIPTIPSPFCRCIENYTGARCEEVFLP	51
		*****.***** * .*****.*****.*****.*****.*****	
hEGFH2 seq	52	GSSIQTksnlFEAFVALAVLVTLIIGAFYFLCRKGHFQRASSVQYDINLVE	102
mEGFH2 seq	52	SSSIPSESnlSAAfVVLAVLLTLTIAALCFLCRKGHLQRASSVQCEISLVE	102
		*** . *** *** *****.*** * * ***** ***** * ***	
hEGFH2 seq	103	TSSTSAHHSHEQH	115
mEGFH2 seq	103	TNNTRTRHSHREH	115
		* * .*** *	

005T80" F4004950

Sequence Range: 1 to 348

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                25                                50
ATG CCA ACA GAT CAC GAA GAG CCC TGT GGT CCC AGT CAC AAG TCG TTT TGC
TAC GGT TGT CTA GTG CTT CTC GGG ACA CCA GGG TCA GTG TTC AGC AAA ACG

                75                                100
CTG AAT GGG GGG CTT TGT TAT GTG ATA CCT ACT ATT CCC AGC CCA TTT TGT
GAC TTA CCC CCC GAA ACA ATA CAC TAT GGA TGA TAA GGG TCG GGT AAA ACA

                125                                150
AGG TGC GTT GAA AAC TAT ACA GGA GCT CGT TGT GAA GAG GTT TTT CTC CCA
TCC ACG CAA CTT TTG ATA TGT CCT CGA GCA ACA CTT CTC CAA AAA GAG GGT

                175                                200
GGC TCC AGC ATC CAA ACT AAA AGT AAC CTG TTT GAA GCT TTT GTG GCA TTG
CCG AGG TCG TAG GTT TGA TTT TCA TTG GAC AAA CTT CGA AAA CAC CGT AAC

                225                                250
GCG GTC CTA GTA ACA CTT ATC ATT GGA GCC TTC TAC TTC CTT TGC AGG AAA
CGC CAG GAT CAT TGT GAA TAG TAA CCT CGG AAG ATG AAG GAA ACG TCC TTT

                275                                300
GGC CAC TTT CAG AGA GCC AGT TCA GTC CAG TAT GAT ATC AAC CTG GTA GAG
CCG GTG AAA GTC TCT CGG TCA AGT CAG GTC ATA CTA TAG TTG GAC CAT CTC

                325
ACG AGC AGT ACC AGT GCC CAC CAC AGT CAT GAA CAA CAC TGA
TGC TCG TCA TGG TCA CGG GTG GTG TCA GTA CTT GTT GTG ACT
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FIGURE 2

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**0-9**

FIGURE 3

FIGURE 3

FIGURE 4

<u>Sample</u>	<u>Experiment 1</u>	<u>Experiment 2</u>
2 (antisense)	0/9	0/10
3 (sense)	3/9	8/8
4 (sense)	7/7	11/11

005750" F4004960